

Sequence Match Listing for 09/954987

RESULT 6
 BE705670/c
 LOCUS BE705670 737 bp mRNA linear EST 12-SEP-2000
 DEFINITION Sc01_11a10_A Sc01_AAFC_ECORC_cold_stressed_winter_rye_seedlings
 Secale cereale cDNA clone Sc01_11a10, mRNA sequence.
 ACCESSION BE705670
 VERSION BE705670.1 GI:10093935
 KEYWORDS EST.
 SOURCE rye.
 ORGANISM Secale cereale
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
 ; Triticeae; Secale.
 REFERENCE 1 (bases 1 to 737)
 AUTHORS Singh, J.A., Piche, C., Couroux, P., De Moors, A., Harris, L.J., Hattori,
 J.I., Ouellet, T., Robert, L.S., Sprott, D. and Tinker, N.A.
 TITLE Expressed Sequence Tags from Cold-Stressed Winter Rye Seedlings
 JOURNAL Unpublished (2000)
 COMMENT Contact: Singh, J.A.
 Eastern Cereal and Oilseed Research Centre
 Agriculture and Agri-food Canada
 KW Neatby Bldg., Central Experimental Farm, Ottawa, Ontario, K1A
 0C6, Canada
 Tel: (613) 759-1662
 Fax: (613) 759-1701
 Email: singhja@em.agr.ca.
 FEATURES Location/Qualifiers
 source 1..737
 /organism="Secale cereale"
 /cultivar="Puma (winter rye)"
 /db_xref="taxon:4550"
 /clone="Sc01_11a10"
 /clone_lib="Sc01_AAFC_ECORC_cold_stressed_winter_rye_seedl
 ings"
 /tissue_type="leaf, crown"
 /dev_stage="seedling three-leaf stage"
 /note="Vector: Bluescript SK-/XhoI-EcoRI; Site_1: Eco RI;
 Site_2: Xho I; Sampled three-leaf seedlings treated for
 one week at 20C, 12 hrs light/day. Library made with
 Stratagene UNIZAP XR Kit/Gigapack III Gold Kit. Lambda
 library is amplified, then mass excised in SOLR cells. "
 BASE COUNT 156 a 189 c 200 g 170 t 22 others
 ORIGIN
 Query Match 55.1%; Score 24.8; DB 12; Length 737;
 Best Local Similarity 80.6%; Pred. No. 46;
 Matches 29; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
 QY 1 CTGCATGGAGTGGCGCCAAAAGTCCCTCCACCTACA 36
 ||| |||| |||||||| || ||||| |||||
 Db 549 CTGAGTGGAGGGCGGCCAAGAGCCCTCCTACTACA 514
 536 531

RESULT 7

BE412777
 LOCUS BE412777 928 bp mRNA linear EST 24-JUL-2000
 DEFINITION MCG008.H03R990625 ITEC MCG Barley Leaf/Culm Library Hordeum vulgare
 cDNA clone MCG008.H03, mRNA sequence.
 ACCESSION BE412777
 VERSION BE412777.1 GI:9410525
 KEYWORDS EST.
 SOURCE Hordeum vulgare.
 ORGANISM Hordeum vulgare
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
 ; Triticeae; Hordeum;
 REFERENCE 1 (bases 1 to 928)
 AUTHORS Anderson,O.A., Appels,R., Bailey,P., Blake,T., Close,T., Cloutier
 ,S., Dubcovsky,J., Feuillet,C., Gale,M., Graner,A., Gustafson,P.,
 Herrmann,R.G., Holton,T., Jacquemin,J.M., Jia,J., Joudrier,P.,
 Langridge,P., Lazo,G.R., Lin,J.J., McGuire,P., Ogihara,Y.,
 Pecchioni,N., Qualset,C., Schuch,W., Selvaraj,G., Shariflou,M.,
 Sorrells,M., Warburton,M. and Wenzel,G.
 TITLE International Triticeae EST Cooperative (ITEC): Production of
 Expressed Sequence Tags for Species of the Triticeae
 JOURNAL Unpublished (2000)
 COMMENT Contact: Graner A
 Institute for Plant Genetics & Crop Plant Research
 Corrensstr. 3, D-06466 Gatersleben GERMANY
 Tel: 49 39482 5521
 Fax: 49 39482 5137
 Email: a_graner@ipk-gatersleben.de
 International Triticeae EST Cooperative (ITEC)
 http://wheat.pw.usda.gov/genome.
 FEATURES Location/Qualifiers
 source 1. 928
 /organism="Hordeum vulgare"
 /db_xref="taxon:4513"
 /clone="MCG008.H03"
 /clone_lib="ITEC MCG Barley Leaf/Culm Library"
 /tissue_type="leaf/culm"
 /dev_stage="etiolated"
 BASE COUNT 237 a 181 c 247 g 254 t 9 others
 ORIGIN
 Query Match 55.1%; Score 24.8; DB 10; Length 928;
 Best Local Similarity 80.6%; Pred. No. 48;
 Matches 29; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
 QY 1 CTGCATGGAGTGC GGCCAAAAGTCCCTCCACCTACA 36
 ||| ||||| ||||| || ||||| |||||
 Db 86 CTGAGTGGAGGGCGGCCAAGAGCCCTCCTACTACA 121
 99 104

RESULT 13
 AQ984126/c
 LOCUS AQ984126 503 bp DNA linear GSS 30-JAN-2000
 DEFINITION RPCI-23-306D11.TV RPCI-23 Mus musculus genomic clone RPCI-23-306D11
 , DNA sequence.
 ACCESSION AQ984126
 VERSION AQ984126.1 GI:6817331
 KEYWORDS GSS.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 503)
 AUTHORS Zhao, S., Nierman, W., Feldblyum, T., Malek, J., Shatsman, S., Akinret,
 B., Levins, M., McGann, S., Tsegaye, G., Geer, K., Krol, M., de Jong, P.
 and Fraser, C.M.
 TITLE Mouse BAC End Sequences from Library RPCI-23
 JOURNAL Unpublished (1999)
 COMMENT Other_GSSs: RPCI-23-306D11.TJ
 Contact: Shaying Zhao
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850, USA
 Tel: 301 838 0200
 Fax: 301 838 0208
 Email: szhao@tigr.org
 Clones are derived from the mouse BAC library RPCI-23. For BAC
 library availability, please contact Pieter de Jong
 (pieter@dejong.med.buffalo.edu). Clones may be purchased from

BACPAC Resources (<http://bacpac.med.buffalo.edu/orderingframe.htm>)
 or from Reseach Genetics (info@resgen.com). BAC end page:
http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
 Plate: 306 row: D column: 11
 Seq primer: T7
 Class: BAC ends.

FEATURES
 source Location/Qualifiers
 1..503
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="RPCI-23-306D11"
 /clone_lib="RPCI-23"
 /sex="Female"
 /lab_host="DH10B"
 /note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1:
 EcoRI; Site_2: EcoRI; Female C57BL/6J mouse kidney and/or
 brain genomic DNA was isolated and partially digested
 with a combination of EcoRI and EcoRI Methylase. Size
 selected DNA was cloned into the pBACe3.6 vector at the
 EcoRI sites. The ligation products were transformed into
 DH10B electrocompetent cells (BRL Life Technologies)."
 BASE COUNT 144 a 125 c 127 g 107 t
 ORIGIN

Query Match 51.6%; Score 23.2; DB 17; Length 503;
 Best Local Similarity 70.5%; Pred. No. 1.7e+02;
 Matches 31; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 2 TGCATGGAGTGC GGCCAAAAGTCCCTCCACCTACATCCCGATAC 45
 | | | | | | | | | | | | | | | | | | | | | | | | | |
 Db 385 TACATGGACCCAGGCCAACAGTTCTTCTCCCCACATCCGGAGAC 342

RESULT 13

T49841

hypothetical protein B24H17.270 [imported] - Neurospora crassa

C;Species: Neurospora crassa

C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 18-Aug-2000

C;Accession: T49841

R;Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura, submitted to the Protein Sequence Database, May 2000

A;Reference number: Z25022

A;Accession: T49841

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-218 <SCH>

A;Cross-references: EMBL:AL356815 GSPDB:GN00116; NCSP:B24H17.270

A;Experimental source: BAC clone B24H17; strain OR74A

C;Genetics:

A;Gene: NCSP:B24H17.270

A;Map position: 6

A;Introns: 8/1; 107/1; 144/1; 180/2

C;Superfamily: Neurospora crassa hypothetical protein B24H17.270

Query Match 38.5%; Score 48.5; DB 2; Length 218;

Best Local Similarity 52.9%; Pred. No. 21;

Matches 9; Conservative 2; Mismatches 5; Indels 1; Gaps 1;

QY 3 RCDHAPNPCME-CGQKS 18

: || | ||: ||||

Db 40 QADHGNEPCLPVCQKS 56

RESULT 2
AF245704
LOCUS AF245704 3352 bp mRNA linear PRI 21-MAR-2001
DEFINITION Homo sapiens toll-like receptor 9 (TLR9) mRNA, complete cds.
ACCESSION AF245704
VERSION AF245704.1 GI:8575528

earliest date June 21 2000

KEYWORDS
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 3352)
AUTHORS Chuang, T.H. and Ulevitch, R.J.
TITLE Cloning and characterization of a sub-family of human toll-like
receptors: hTLR7, hTLR8 and hTLR9
JOURNAL Eur. Cytokine Netw. 11 (3), 372-378 (2000)
MEDLINE 20477807
PUBMED 11022120
REFERENCE 2 (bases 1 to 3352)
AUTHORS Chuang, T.-H.H. and Ulevitch, R.J.
TITLE Direct Submission
JOURNAL Submitted (15-MAR-2000) Immunology, The Scripps Research Institute,
10550 North Torrey Pines Road, La Jolla, CA 92037, USA

FEATURES
source Location/Qualifiers
1..3352
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="3"
/map="3p21"
/tissue_type="placenta"
gene 1..3352
/gene="TLR9"
CDS 145..3243
/gene="TLR9"
/codon_start=1
/product="toll-like receptor 9"
/protein_id="AAF78037.1"
/db_xref="GI:8575529"
/translation="MGFCRSALHPLSLLVQAIMLAMTLALGTLPAFLPCELQPHGLVN
CNWLFKLSVPHFSMAAPRGVNTSLSLSSNRHHHLDSDFAHLPSLRHLNLKWCNCPVVG
LSPMHFPCHMTIEPSTFLAVPTLEELNLSYNNIMTVPALPKSLISLSLSTNIMLDS
ASLAGLHALRFLFMDGNCYYKNPCRALEVPAGALLGLGNLTHLSLKYNNLTVVPRNL
PSSLEYLLLSYNRIVKLAPEDLANLTALRVLDVGGNCRRCDHAPNPMCECPRHFPQLH
PDTFSHLSRLEGLVLKSSLSWLNASWFRGLGNLRVLDLSENFLYKCIKTKAFQGLT
QLRKLNLSPNYQKRVSPFAHLSLAPSPGSLVALKELDMHGIFFRSLDETTLRPLARLPM
LQTLRLQMNFINQAQIGIFRAFPGLRYVDLSNDRISGASELTATMGADGGKQVWLQP
GDLAPAPVDTTPSSEDFRPNCSLTNFTLDLSRNNLTVTQPEMFAQLSHLQCLRLSHNCI
SQAVNGSQFLPLTGLQVLDLSRNKLDLYHEHSFTLPRLEALDLSYNSQPFQMGQVGH
NFSFVAHLRTLRLHLSLAHNNIHSQVSQQLCSTSLRALDFSGNALGHMMAEGDLYLHFF
QGLSGLIWLDSLQNRHLTLLPQTLRNLPKSLQVLRRLRNLAFKWWSLHFLPKLEVL
DLAGNRLKALTNGSLPAGTRRLRLDVSNCNISFVAPGFFSKAKELRELNLNANALKT
DHSWFGPLASALQILDVSNPLHCAGAAFMDFLLEVQAAVPGVPSRVKCGSPGQLQG
LSIFAQDLRLCLDEALSWDCFALSLLAVALGLGVPLHHLGCGWDLWYCFHLCCLAWLPW
RGRQSGRDEDALPYDAFVVFVKTSADAVWVYNELRGQLEECRGRWALRLCLEERDNL
PGKTLFENLWASVYGSRKTLFVLAHTDRVSGLLRASPLLAQORLLEDRKDVVVLVILS
PDGRRSRYVRLRQLRCQSVLLWPHQPSGQSFVAQLGMALTRDNHHFYNNRNCQGGPT
AE"

BASE COUNT 585 a 1196 c 891 g 680 t
ORIGIN

Query Match 99.5%; Score 3080; DB 9; Length 3352;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 3086; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 1 ATGGGTTTCTGCCGAGCGCCCTGCACCCGCTGTCTCTCTGGTGCAGGCCATCATGCTG 60
|||
Db 145 ATGGGTTTCTGCCGAGCGCCCTGCACCCGCTGTCTCTCTGGTGCAGGCCATCATGCTG 204
Qy 61 GCCATGACCTGGCCCTGGGTACCTTGCTGCTCTCTACCTGTGAGCTCCAGCCCCAC 120

23 10:03:23 2003

70

Qy 2281 CCTCTGCACTGCGCCTGTGGGGCGGCCTTTATGGACTTCCTGCTGGAGGTGCAGGCTGCC 2340
 Db 2425 CCTCTGCACTGCGCCTGTGGGGCGGCCTTTATGGACTTCCTGCTGGAGGTGCAGGCTGCC 2484
 Qy 2341 GTGCCCCGGTCTGCCCAGCCGGTGAAGTGTGGCAGTCCGGGCCAGCTCCAGGGCCTCAGC 2400
 Db 2485 GTGCCCCGGTCTGCCCAGCCGGTGAAGTGTGGCAGTCCGGGCCAGCTCCAGGGCCTCAGC 2544
 Qy 2401 ATCTTTGCACAGGACCTGCGCCTCTGCCTGGATGAGGCCCTCTCCTGGGACTGTTTCGCC 2460
 Db 2545 ATCTTTGCACAGGACCTGCGCCTCTGCCTGGATGAGGCCCTCTCCTGGGACTGTTTCGCC 2604
 Qy 2461 CTCTCGCTGCTGGCTGTGGCTCTGGGCCTGGGTGTGCCATGCTGCATCACCTCTGTGGC 2520
 Db 2605 CTCTCGCTGCTGGCTGTGGCTCTGGGCCTGGGTGTGCCATGCTGCATCACCTCTGTGGC 2664
 Qy 2521 TGGGACCTCTGGTACTGCTTCCACCTGTGCCTGGCCTGGCTTCCCTGGCGGGGGCGGCAA 2580
 Db 2665 TGGGACCTCTGGTACTGCTTCCACCTGTGCCTGGCCTGGCTTCCCTGGCGGGGGCGGCAA 2724
 Qy 2581 AGTGGGCGAGATGAGGATGCCCTGCCCTACGATGCCTTCGTGGTCTTCGACAAAACGCAG 2640
 Db 2725 AGTGGGCGAGATGAGGATGCCCTGCCCTACGATGCCTTCGTGGTCTTCGACAAAACGCAG 2784
 Qy 2641 AGCGCAGTGGCAGACTGGGTGTACAACGAGCTTCGGGGGCGAGCTGGAGGAGTCCCGTGGG 2700
 Db 2785 AGCGCAGTGGCAGACTGGGTGTACAACGAGCTTCGGGGGCGAGCTGGAGGAGTCCCGTGGG 2844
 Qy 2701 CGCTGGGCACTCCGCTGTGCCTGGAGGAACGCGACTGGCTGCCTGGCAAAACCTCTTT 2760
 Db 2845 CGCTGGGCACTCCGCTGTGCCTGGAGGAACGCGACTGGCTGCCTGGCAAAACCTCTTT 2904
 Qy 2761 GAGAACCTGTGGGCCTCGGTCTATGGCAGCCGCAAGACGCTGTTTGTGCTGGCCACACG 2820
 Db 2905 GAGAACCTGTGGGCCTCGGTCTATGGCAGCCGCAAGACGCTGTTTGTGCTGGCCACACG 2964
 Qy 2821 GACCGGGTCAGTGGTCTCTTGCGCCAGCTTCCTGCTGGCCAGCAGCGCTGCTGGAG 2880
 Db 2965 GACCGGGTCAGTGGTCTCTTGCGCCAGCTTCCTGCTGGCCAGCAGCGCTGCTGGAG 3024
 Qy 2881 GACCGCAAGGACGTCGTGGTGTGGTATCCTGAGCCCTGACGGCCGCGCTCCCGCTAC 2940
 Db 3025 GACCGCAAGGACGTCGTGGTGTGGTATCCTGAGCCCTGACGGCCGCGCTCCCGCTAC 3084
 Qy 2941 GTGCGGCTGCGCCAGCGCCTCTGCCGCCAGAGTGTCTCTCTGCGCCCAACAGCCAGT 3000
 Db 3085 GTGCGGCTGCGCCAGCGCCTCTGCCGCCAGAGTGTCTCTCTGCGCCCAACAGCCAGT 3144
 Qy 3001 GGTGAGCGCAGCTTCTGGGCCAGCTGGGCATGGCCCTGACCAGGGACACCACTTC 3060
 Db 3145 GGTGAGCGCAGCTTCTGGGCCAGCTGGGCATGGCCCTGACCAGGGACACCACTTC 3204
 Qy 3061 TATAACCGGAACCTTCTGCCAGGGACCCACGGCCGAA 3096
 Db 3205 TATAACCGGAACCTTCTGCCAGGGACCCACGGCCGAA 3240